QUANTITATIVE GENETICS OF RESISTANCE TO NET BLOTCH OF BARLEY (*Hordeum vulgare* L.)

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ABSTRACT

A half diallel cross was made amongst five barley (*Hordeum vulgare* L.) genotypes (Zephyr, Hassan, Mata, Kaniere and Manchuria) which exhibited differential resistance to net blotch disease, incited by the fungus, *Drechslera teres*.

The 15 genotypes (5 parents and 10 F_1's) were grown to physiological maturity under two nitrogen regimes (20 mg $10^{-3}m^{-3}$ and 105 mg $10^{-3}m^{-3}$ N), 14 hour photoperiod, light intensity of 170Wm^{-2}PAR, 22°C (day)/16°C (night) and relative humidities of 70% (first seven weeks) and 95 to 100%.

All genotypes were first inoculated (9,000 conidia $10^{-6}m^{-3}$) at 14 days and thereafter ten times at approximately weekly intervals. Infection occurred only in the high nitrogen environment. Absence of net blotch at the lower nitrogen level was probably due to insufficient plant nitrogen concentrations for growth of the fungus.

The procedures of Mather and Jinks were used to analyse the half diallel cross for net blotch resistance of the following intact plant parts: (1) top canopy (2) bottom canopy (3) flag leaf and (4) second leaf. Resistance of leaf sections in petri dishes was also analysed.

Biometrical analyses for all net blotch data sets showed that additivity was of much greater importance than dominance in controlling resistance. Epistasis and/or correlated gene distributions were trivial. Resistance was conditioned by a partially dominant, single effective factor which was suggested as one gene. Heritability estimates were moderate.

In the high nitrogen environments, net blotch had no significant effect on plant height, tillers per plant, spikelet and grain numbers per ear, grain yield, 100 kernel weight and intensity of physiological brown

spot. However heading date of diseased plants was significantly earlier than for fungicide treated plants.

Nitrogen concentration had a marked effect on most characters. Significant genotype-nitrogen (G x E) interactions occurred for plant height, spikelet number per ear, grain yield, 100 kernel weight and physiological brown spot.

Further biometrical analyses showed that additivity was most important for plant height, tillers per plant, spikelet and grain numbers per ear, and physiological brown spot. Dominance was noteworthy for heading date, grain yield and 100 kernel weight. Epistasis was relatively unimportant.

Keywords: biometrics, barley, diallel analysis, disease resistance, growth stages, inoculation, intensity, leaf area diagrams, net blotch, pathogen, quantitative genetics, susceptibility.

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INTRODUCTION

Barley (*Hordeum vulgare L.*) is susceptible to many diseases (Nyvall, 1979) which may severely affect the quantity and quality of the harvested product. A disease which has received considerable attention, particularly in the last decade, is net blotch (Shipton *et al.*, 1973; Arnst *et al.*, 1978). This is a seed-borne (Neergaard, 1977), foliage disease caused by the fungus *Drechslera teres* (Sacc.) Shoem. (syn. *Helminthosporium teres*), conidial state of *Pyrenophora teres* (Died.) Drechsler. Net blotch is widespread, occurring wherever barley is grown in the humid, temperate regions of the world (Dickson, 1956). In New Zealand, its presence was first recorded by Dingley (1969).

Grain yield losses due to net blotch have been of economic significance in many barley growing regions of the world and yield reductions of up to 50 per cent are documented (Shipton *et al.*, 1973). The most important adverse effect of the disease is grain shrivelling as measured by reduction in 1,000 grain weight (Buchannon and Wallace, 1962; Hampton and Arnst, 1978). Other agronomic features which may be affected adversely by *D. teres* attack include tillering (Hampton, 1977), straw stiffness (Hampton, 1977) and carbohydrate content of grain (Shipton, 1966).

The dramatic yield losses attributable to net blotch have prompted extensive investigation into effective methods of disease control. Numerous studies have been conducted overseas to identify genetic stocks which exhibit a high degree of resistance to net blotch (Shipton *et al.*, 1973), with a view to their possible inclusion in breeding programmes. Qualitative inheritance of resistance has been studied

(Schaller, 1955; Mode and Schaller, 1958; Khan and Boyd, 1969a). However, the findings are conflicting (Bockelman *et al.*, 1977) and further investigation on inheritance of net blotch resistance is warranted. Results from qualitative studies are discussed shortly.

Environmental conditions may markedly affect the incidence and severity of net blotch (Shipton *et al.*, 1973). Studies on the effect of nitrogen nutrition on host resistance to *D. teres* are very limited and demonstrate both an increase (Singh, 1963; Piening, 1967) and decrease (Piening, 1967) in resistance with increasing nitrogen levels.

The main objective of the present study is to estimate quantitative genetic statistics for resistance to net blotch under controlled environmental conditions, using a diallel analysis (Griffing, 1956a, b; Mather and Jinks, 1971, 1977). These statistics cannot be estimated from qualitative studies, as conducted previously.

Further objectives are:

1) Examination of change in host resistance to net blotch with variation in nitrogen concentration, including estimation of genotype - nitrogen interaction (G x E), and
2) Investigation of the adverse effects of net blotch and formulation of a relationship between net blotch intensity and grain yield loss (disease - yield loss model).